```
      Set  Items  Description
      ---  -----  -----------
?s hairpin (s) activat? (s) (trans or cis)
Processing
Processed  10 of  37 files ...
Processing
Completed processing all files
          34335  HAIRPIN
        4787005  ACTIVAT?
         644669  TRANS
         425724  CIS
      S1     198  HAIRPIN (S) ACTIVAT? (S) (TRANS OR CIS)
?s s s1 and (chang? (3n) conformat?)
Processing
Processed  10 of  37 files ...
Completed processing all files
               0  S S1
         8932535  CHANG?
         1076821  CONFORMAT?
          146715  CHANG?(3N)CONFORMAT?
      S2       0  S S1 AND (CHANG? (3N) CONFORMAT?)
?s hairpin (s) activat? (s) hybridiz?
Processing
Processed  10 of  37 files ...
Completed processing all files
          34335  HAIRPIN
        4787005  ACTIVAT?
         936019  HYBRIDIZ?
      S3      44  HAIRPIN (S) ACTIVAT? (S) HYBRIDIZ?
?rd
...completed examining records
      S4      28  RD (unique items)
?show files;ds;t/3,k/all
File   5:Biosis Previews(R) 1969-2004/Feb W3
         (c) 2004 BIOSIS
File   6:NTIS 1964-2004/Feb W4
         (c) 2004 NTIS, Intl Cpyrght All Rights Res
File   8:Ei Compendex(R) 1970-2004/Feb W2
         (c) 2004 Elsevier Eng.  Info. Inc.
File  34:SciSearch(R) Cited Ref Sci 1990-2004/Feb W2
         (c) 2004 Inst for Sci Info
File  65:Inside Conferences 1993-2004/Feb W3
         (c) 2004 BLDSC all rts. reserv.
File  71:ELSEVIER BIOBASE 1994-2004/Feb W2
         (c) 2004  Elsevier Science B.V.
File  73:EMBASE 1974-2004/Feb W3
         (c) 2004 Elsevier Science B.V.
File  94:JICST-EPlus 1985-2004/Feb W2
         (c)2004 Japan Science and Tech Corp(JST)
File  98:General Sci Abs/Full-Text 1984-2004/Jan
         (c) 2004 The HW Wilson Co.
File  99:Wilson Appl. Sci & Tech Abs 1983-2004/Jan
         (c) 2004 The HW Wilson Co.
File 135:NewsRx Weekly Reports 1995-2004/Feb W3
         (c) 2004 NewsRx
File 143:Biol. & Agric. Index 1983-2004/Jan
         (c) 2004 The HW Wilson Co
File 144:Pascal 1973-2004/Feb W2
         (c) 2004 INIST/CNRS
File 155:MEDLINE(R) 1966-2004/Feb W3
         (c) format only 2004 The Dialog Corp.
File 172:EMBASE Alert 2004/Feb W2
         (c) 2004 Elsevier Science B.V.
File 266:FEDRIP 2004/Jan
         Comp & dist by NTIS, Intl Copyright All Rights Res
File 315:ChemEng & Biotec Abs 1970-2004/Jan
```

(c) 2004 DECHEMA
File 357:Derwent Biotech Res. _1982-2004/Feb W4
(c) 2004 Thomson Derwent & ISI
File 358:Current BioTech Abs 1983-2004/Jan
(c) 2004 DECHEMA
File 369:New Scientist 1994-2004/Feb W3
(c) 2004 Reed Business Information Ltd.
File 370:Science 1996-1999/Jul W3
(c) 1999 AAAS
File 399:CA SEARCH(R) 1967-2004/UD=14008
(c) 2004 American Chemical Society
File 434:SciSearch(R) Cited Ref Sci 1974-1989/Dec
(c) 1998 Inst for Sci Info
File 40:Enviroline(R) 1975-2004/Dec
File 50:CAB Abstracts 1972-2004/Jan
(c) 2004 CAB International
File 103:Energy SciTec 1974-2004/Feb B1
(c) 2004 Contains copyrighted material
File 156:ToxFile 1965-2004/Feb W3
(c) format only 2004 The Dialog Corporation
File 162:Global Health 1983-2004/Jan
(c) 2004 CAB International
File 305:Analytical Abstracts 1980-2004/Jan W2
(c) 2004 Royal Soc Chemistry
File 35:Dissertation Abs Online 1861-2004/Jan
(c) 2004 ProQuest Info&Learning
File 48:SPORTDiscus 1962-2004/Feb
(c) 2004 Sport Information Resource Centre
File 91:MANTIS(TM) 1880-2003/Feb
2001 (c) Action Potential
File 149:TGG Health&Wellness DB(SM) 1976-2004/Feb W2
(c) 2004 The Gale Group
File 159:Cancerlit 1975-2002/Oct
(c) format only 2002 Dialog Corporation
File 164:Allied & Complementary Medicine 1984-2004/Feb
(c) 2004 BLHCIS
File 444:New England Journal of Med. 1985-2004/Feb W4
(c) 2004 Mass. Med. Soc.
File 467:ExtraMED(tm) 2000/Dec
(c) 2001 Informania Ltd.

Set	Items	Description
S1	198	HAIRPIN (S) ACTIVAT? (S) (TRANS OR CIS)
S2	0	S S1 AND (CHANG? (3N) CONFORMAT?)
S3	44	HAIRPIN (S) ACTIVAT? (S) HYBRIDIZ?
S4	28	RD (unique items)

>>>KWIC option is not available in file(s): 399

4/3,K/1 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0012974413 BIOSIS NO.: 200100146252
Immobilization of oligodeoxyribonucleotides with multiple anchors to microchips
AUTHOR: Zhao Xiaodong; Nampalli Satyam; Serino Anthony J; Kumar Shiv (Reprint)
AUTHOR ADDRESS: Amersham Pharmacia Biotech Inc., 800 Centennial Avenue, Piscataway, NJ, 08855, USA**USA
JOURNAL: Nucleic Acids Research 29 (4): p955-959 February 15, 2001 2001
MEDIUM: print
ISSN: 0305-1048
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Facile modification of oligodeoxyribonucleotides is required for

efficient immobilization to a pre-*activated* glass surface. This report presents an oligodeoxyribonucleotide which contains a *hairpin* stem-loop structure with multiple phosphorothioate moieties in the loop. These moieties are used to anchor the oligo to glass slides that are pre-*activated* with bromoacetamidopropylsilane. The efficiency of the attachment reaction was improved by increasing the number of phosphorothioates in the loop, as shown in the remarkable enhancement of template *hybridization* and single base extension through catalysis by DNA polymerase. The loop and stem presumably serve as lateral spacers between neighboring oligodeoxyribonucleotides and as a linker arm between the glass surface and the single-stranded sequence of interest. The oligodeoxyribonucleotides of this *hairpin* stem-loop architecture with multiple phosphorothioate moieties have broad application in DNA chip-based gene analysis.

4/3,K/2 (Item 2 from file: 5)

0012876537 BIOSIS NO.: 200100048376

Characterization of the interaction between alphaCP2 and the 3'-untranslated region of collagen alpha1(I) mRNA

AUTHOR: Lindquist Jeffrey N; Kauschke Stefan G; Stefanovic Branko; Burchardt Elmar R; Brenner David A (Reprint)
AUTHOR ADDRESS: Department of Medicine and Department of Biochemistry and Biophysics, University of North Carolina at Chapel Hill, Chapel Hill, NC, 27599-7038, USA**USA

JOURNAL: Nucleic Acids Research 28 (21): p4306-4316 November 1, 2000 2000
MEDIUM: print
ISSN: 0305-1048
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: *Activated* hepatic stellate cells produce increased type I collagen in hepatic fibrosis. The increase in type I collagen protein results from an increase in mRNA levels...

...mRNA stability. Protein-RNA interactions in the 3'-UTR of the collagen alpha1(I) mRNA correlate with stabilization of the mRNA during hepatic stellate cell *activation*. A component of the binding complex is alphaCP2. Recombinant alphaCP2 is sufficient for binding to the 3'-UTR of collagen alpha1(I). To characterize the...

...we demonstrate a system for detecting protein-nucleotide interactions that is suitable for high throughput assays using molecular beacons. Molecular beacons, developed for DNA-DNA *hybridization*, are oligonucleotides with a fluorophore and quencher brought together by a *hairpin* sequence. Fluorescence increases when the *hairpin* is disrupted by binding to an antisense sequence or interaction with a protein. Molecular beacons displayed a similar high affinity for binding to recombinant alphaCP2...

4/3,K/3 (Item 3 from file: 5)

0011835317 BIOSIS NO.: 199900094977

Dual blockade of cyclic AMP response element- (CRE) and AP-1-directed transcription by CRE-transcription factor decoy oligonucleotide. Gene-specific inhibition of tumor growth

AUTHOR: Park Yun Gyu; Nesterova Maria; Agrawal Sudhir; Cho-Chung Yoon S (Reprint)
AUTHOR ADDRESS: National Institutes Health, NCI, Build. 10, Room 5B05, Bethesda, MD 20892-1750, USA**USA

JOURNAL: Journal of Biological Chemistry 274 (3): p1573-1580 Jan. 15, 1999
1999
MEDIUM: print
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

...ABSTRACT: cells as decoy cis-elements to bind the factors and alter gene expression. The CRE (cyclic AMP response element)transcription factor complex is a pleiotropic *activator* that participates in the induction of a wide variety of cellular and viral genes. Because the CRE cis-element, TGACGTCA, is palindromic, a synthetic single-stranded oligonucleotide composed of the CPE sequence self-*hybridizes* to form a duplex/*hairpin*. Herein we report that the CRE-palindromic oligonucleotide can penetrate into cells, compete with CRE enhancers for binding transcription factors, and specifically interfere with CRE...

4/3,K/4 (Item 4 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0008417797 BIOSIS NO.: 199294119638
RNA PROCESSING MODULATES THE EXPRESSION OF THE ARCDABC OPERON IN PSEUDOMONAS-AERUGINOSA
AUTHOR: GAMPER M (Reprint); GANTER B; POLITO M R; HAAS D
AUTHOR ADDRESS: MIKROBIOLOGISCHES INST, EIDGENOSSISCHE TECHNISCHE HOCHSCHULE, CH-8092 ZURICH, SWITZ**SWITZERLAND
JOURNAL: Journal of Molecular Biology 226 (4): p943-957 1992
ISSN: 0022-2836
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

...ABSTRACT: operon encoding the enzymes of the arginine deliminase pathway. The co-ordinate, anaerobic induction of these enzymes requires the FNR-like regulatory protein ANR, which *activates* the arc promoter lying upstream from arcD. By Northern *hybridization* experiments, three abundant arcA, arcAB and arcABC transcripts and three minor arcDA, arcDAB and arcDABC transcripts could be detected. The 5' ends of the arcA...

...cuts within arcD. Deletion of the putative intergenic stem-loop structures did not result in a dramatic loss of arc mRNA stability. Thus, the intergenic *hairpin* structures do not contribute importantly to the overall mRNA stability; they might act primarily as partial transcription terminators and locally protect the 3' ends from...

4/3,K/5 (Item 5 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0002923199 BIOSIS NO.: 198069037186
ENZYMOLOGICAL CHARACTERIZATION OF KB CELL DNA POLYMERASE ALPHA 3. THE POLYMERIZATION REACTION WITH SINGLE STRANDED DNA
AUTHOR: FISHER P A (Reprint); KORN D
AUTHOR ADDRESS: LAB EXP ONCOL, DEP PATHOL, STANFORD UNIV SCH MED, STANFORD, CALIF 94305, USA**USA
JOURNAL: Journal of Biological Chemistry 254 (21): p11040-11046 1979
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

...ABSTRACT: reaction demonstrates an apparent Km for DNA of .apprx. 10 .mu.M and a Vmax that ranges from 10-30% of that determined with

optimally *activated* DNA. Both kinetic parameters depended on the ratio of 3'-hydroxyl termini to total single strand nucleotide in the primer-template population. The effect of spermidine on the single strand reaction is similar to that observed with *activated* DNA, resulting in marked increases in apparent Km and Vmax. The product of the polymerization reaction is covalently linked to the template in a *hairpin* structure, but the primer terminus is not in a stably base-paired configuration prior to the reaction. The reaction of polymerase-.alpha. with single strand fragments prepared from restriction digests of several viral DNA molecules revealed patterns of preferential fragment utilization. By restriction mapping and Southern *hybridization* analyses, it was shown that the apparent selectivity of the enzyme was not due to recognition of specific DNA sequence, but rather appeared to reflect...

4/3,K/6 (Item 1 from file: 34)

08622012 Genuine Article#: 308QM No. References: 40

Title: Detection and characterization of defective interfering RNAs associated with the cocksfoot mottle sobemovirus

Author(s): Makinen K (REPRINT) ; Generozov E; Arshava N; Kaloshin A; Morozov S; Zavriev S
Corporate Source: UNIV HELSINKI,INST BIOTECHNOL/FIN-00014 HELSINKI//FINLAND/ (REPRINT); RUSSIAN ACAD AGR SCI,INST AGR BIOTECHNOL/MOSCOW 127550//RUSSIA/; MOSCOW MV LOMONOSOV STATE UNIV,BELOZERSKY INST PHYSICOCHEM BIOL/MOSCOW 119899//RUSSIA/

Journal: MOLECULAR BIOLOGY, 2000, V34, N2 (MAR-APR), P291-296
ISSN: 0026-8933 Publication date: 20000300
Publisher: PLENUM PUBL CORP, CONSULTANTS BUREAU, 233 SPRING ST, NEW YORK, NY 10013
Language: English Document Type: ARTICLE (ABSTRACT AVAILABLE)

Abstract: A new RNA of about 900 nt was found in the virions of cocksfoot mottle virus (CfMV) and in infected plants by RNA *hybridization* and RT-PCR. Structural features suggested that this RNA is a defective interfering RNA (diRNA). The CfMV diRNA was shown to consist of a 35-nt 5'-terminal genomic region, which formed a *hairpin*, and a 3'-terminal genomic region, which included the coat protein (CP) gene lacking the first 120 nt. In vitro translation of the diRNA started at the third Met codon to produce truncated CP. The CfMV diRNA was assumed to trans-*activate* synthesis of the CP subgenomic RNA (sgRNA).

4/3,K/7 (Item 2 from file: 34)

04857782 Genuine Article#: UM693 No. References: 50

Title: OXIDATION OF DNA HAIRPINS BY OXORUTHENIUM(IV) - EFFECTS OF STERICS AND SECONDARY STRUCTURE

Author(s): CARTER PJ; CHENG CC; THORP HH
Corporate Source: UNIV N CAROLINA,DEPT CHEM,CB 3290/CHAPEL HILL//NC/27599; UNIV N CAROLINA,DEPT CHEM/CHAPEL HILL//NC/27599

Journal: INORGANIC CHEMISTRY, 1996, V35, N11 (MAY 22), P3348-3354
ISSN: 0020-1669
Language: ENGLISH Document Type: ARTICLE (Abstract Available)

Abstract: The effects of steric hindrance on the oxidation of DNA by polypyridyl oxoruthenium(IV) complexes have been investigated. The complexes oxidize DNA by *activation* either of the 1' ribose C-H bond or by oxo transfer to the guanine nucleobase. A method is presented for determining the relative rates of *activation* of individual sites from the dependence of the extent of cleavage on the oxidant concentration. This analysis shows that *hybridization* of the labeled strand to its

complement attenuates the rate of oxidation of guanine more effectively than the rate of sugar oxidation. Accordingly, higher ratios of guanine/sugar oxidation are observed in single strands. Among the individual guanine residues, however, the relative reactivities ale not altered by *hybridization*; a similar result is obtained for sugar oxidation. This result implies that sequence-dependent chemical reactivity is partly responsible for the different extents of cleavage observed within the sequence. The ability of *hybridization* to protect guanine from oxidation is also apparent in *hairpin* studies, where the stem guanines are much less reactive than the loop guanines, and altered sugar conformations in the loop lead to modulated reactivity. Finally...

4/3,K/8 (Item 1 from file: 71)
DIALOG(R)File 71:ELSEVIER BIOBASE

01602859 2000262708
Characterization of the interaction between alphaCPinf 2 and the 3'-untranslated region of collagen alpha1(I) mRNA
Lindquist J.N.; Kauschke S.G.; Stefanovic B.; Burchardt E.R.; Brenner D.A.
ADDRESS: D.A. Brenner, Department of Medicine, Dept. of Biochemistry/Biophysics, University of North Carolina, Chapel Hill, NC 27599-7038, United States
EMAIL: dab@med.unc.edu
Journal: Nucleic Acids Research, 28/21 (4306-4316), 2000, United Kingdom
PUBLICATION DATE: November 1, 2000
CODEN: NARHA
ISSN: 0305-1048
DOCUMENT TYPE: Article
LANGUAGES: English SUMMARY LANGUAGES: English
NO. OF REFERENCES: 30

Activated hepatic stellate cells produce increased type I collagen in hepatic fibrosis. The increase in type I collagen protein results from an increase in mRNA levels...

...mRNA stability. Protein-RNA interactions in the 3'-UTR of the collagen alpha1(I) mRNA correlate with stabilization of the mRNA during hepatic stellate cell *activation*. A component of the binding complex is alphaCPinf 2. Recombinant alphaCPinf 2 is sufficient for binding to the 3'-UTR of collagen alpha1(I). To...

...we demonstrate a system for detecting protein-nucleotide interactions that is suitable for high throughput assays using molecular beacons. Molecular beacons, developed for DNA-DNA *hybridization*, are oligonucleotides with a fluorophore and quencher brought together by a *hairpin* sequence. Fluorescence increases when the *hairpin* is disrupted by binding to an antisense sequence or interaction with a protein. Molecular beacons displayed a similar high affinity for binding to recombinant alphaCPinf...

4/3,K/9 (Item 2 from file: 71)
DIALOG(R)File 71:ELSEVIER BIOBASE

01101821 1999029464
Dual blockade of cyclic AMP response element- (CRE) and AP-1-directed transcription by CRE-transcription factor decoy oligonucleotide: Gene-specific inhibition of tumor growth
Yun Gyu Park; Nesterova M.; Agrawal S.; Cho-Chung Y.S.
ADDRESS: Y.S. Cho-Chung, National Institutes of Health, NCI, Bldg. 10, Bethesda, MD 20892-1750, United States
EMAIL: chochung@helix.nih.gov
Journal: Journal of Biological Chemistry, 274/3 (1573-1580), 1999, United

States
PUBLICATION DATE: January 15, 1999
CODEN: JBCHA
ISSN: 0021-9258
DOCUMENT TYPE: Article
LANGUAGES: English SUMMARY LANGUAGES: English
NO. OF REFERENCES: 33

...cells as decoy cis-elements to bind the factors and alter gene expression. The CRE (cyclic AMP response element)transcription factor complex is a pleiotropic *activator* that participates in the induction of a wide variety of cellular and viral genes. Because the CRE cis-element, TGACGTCA, is palindromic, a synthetic single-stranded oligonucleotide composed of the CRE sequence self- *hybridizes* to form a duplex/*hairpin*. Herein we report that the CRE- palindromic oligonucleotide can penetrate into cells, compete with CRE enhancers for binding transcription factors, and specifically interfere with CRE...

4/3,K/10 (Item 1 from file: 73)
DIALOG(R)File 73:EMBASE

11055921 EMBASE No: 2000405507
Characterization of the interaction between alphaCPSUB2 and the 3'-untranslated region of collagen alpha1(I) mRNA
Lindquist J.N.; Kauschke S.G.; Stefanovic B.; Burchardt E.R.; Brenner D.A.
D.A. Brenner, Department of Medicine, Dept. of Biochemistry/Biophysics, University of North Carolina, Chapel Hill, NC 27599-7038 United States
AUTHOR EMAIL: dab@med.unc.edu
Nucleic Acids Research (NUCLEIC ACIDS RES.) (United Kingdom) 01 NOV 2000, 28/21 (4306-4316)
CODEN: NARHA ISSN: 0305-1048
DOCUMENT TYPE: Journal ; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH
NUMBER OF REFERENCES: 30

Activated hepatic stellate cells produce increased type I collagen in hepatic fibrosis. The increase in type I collagen protein results from an increase in mRNA levels...

...mRNA stability. Protein-RNA interactions in the 3'-UTR of the collagen alpha1(I) mRNA correlate with stabilization of the mRNA during hepatic stellate cell *activation*. A component of the binding complex is alphaCPSUB2. Recombinant alphaCPSUB2 is sufficient for binding to the 3'-UTR of collagen alpha1(I). To characterize the...

...we demonstrate a system for detecting protein-nucleotide interactions that is suitable for high throughput assays using molecular beacons. Molecular beacons, developed for DNA-DNA *hybridization*, are oligonucleotides with a fluorophore and quencher brought together by a *hairpin* sequence. Fluorescence increases when the *hairpin* is disrupted by binding to an antisense sequence or interaction with a protein. Molecular beacons displayed a similar high affinity for binding to recombinant alphaCPSUB2...

4/3,K/11 (Item 1 from file: 266)
DIALOG(R)File 266:FEDRIP

00315804
IDENTIFYING NO.: 1Z01BC10268-03 AGENCY CODE: CRISP
CRE-PALINDROMIC OLIGONUCLEOTIDE AS A TRANSCRIPTION FACTOR DECOY AND AN INHIBITOR
PRINCIPAL INVESTIGATOR: CHO CHUNG, YOON

SPONSORING ORG.: DIVISION OF BASIC SCIENCES - NCI
FY : 1999

...SUMMARY: cells as decoy cis- elements to bind the factor and alter gene transcription. The CRE (cyclic AMP response element)-transcription factor complex is a pleiotropic *activator* that participates in the induction of a wide variety of cellular and viral genes. Because the CRE cis-element TGACGTCA is palindromic, a synthetic single stranded oligonucleotide composed of the CRE sequence, which will self-*hybridize* to form either a duplex or *hairpin*, when introduced into a cell, can act as a decoy for the transcription factor. We have investigated the CRE-palindromic and -*hairpin* forming oligonucleotides as transcription factor decoys and the biological effects thereof. Herein we report that the CRE- palindromic oligonucleotide penetrated into cells, competed with CRE ...

4/3,K/12 (Item 2 from file: 266)
DIALOG(R)File 266:FEDRIP

00315652
IDENTIFYING NO.: 1Z01BC08281-20 AGENCY CODE: CRISP
Mechanism of cAMP-growth regulatory function
PRINCIPAL INVESTIGATOR: CHO-CHUNG, Y S
SPONSORING ORG.: DIVISION OF BASIC SCIENCES - NCI
FY : 2002

...SUMMARY: diffrentiation. cAMP regulates a striking number of physiologic processes, including intermediary metabolism, cellular proliferation, and neuronal signaling by altering basic pattrens of gene expression via *activation* of cAMP response element (CRE)-directed transcription. The mechanism of the CRE-directed transcription in cell proliferation, however, is largely unexplored. To elucidate the role...

... cell proliferation, we used transcription factor-decoy oligonucleotide approach. Our studies revealed that a synthetic single-stranded oligonucleotide composed of the CRE sequence, which self-*hybridizes* to form a duplex/*hairpin* , can penetrate into cells, compete with CRE enhancers for binding transcription factors and specifically interfere with CRE- and Ap-1-directed transcription in vivo . This...
... transcription of array of genes. Recent development of high throughput DNA microarray enables parallel analysis of expression profiles of thousands of genes in a single *hybridization* for complex biological systems. Using DNA microarrays, we have conducted a systematic charaterization of gene expression in cells exposed to antisense, either exogenously or endogenously...

... antisense targeted to protein kinase A RIa alters expression of the clusters of coordinately expressed genes at a specific stage of cell growth, differentiation, and *activation* . The genes that define the proliferation-transformation signature are down-regulated, whereas those that define the differentiation-reverse transformation signature are up-regulated in antisense...

4/3,K/13 (Item 1 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.

0330085 DBR Accession No.: 2004-02377 PATENT
New oligonucleotide probe for detecting a target polynucleotide comprising first and second targeting portions and a proximity-modulated signal generating system, useful for detecting e.g., gastrointestinal cancer - DNA probe for disease diagnosis
AUTHOR: LYLES F E
PATENT ASSIGNEE: NANOCYTOMETRY CORP 2003

PATENT NUMBER: WO 200395666 PATENT DATE: 20031120 WPI ACCESSION NO.: 2004-012132 (200401)
PRIORITY APPLIC. NO.: US 378006 APPLIC. DATE: 20020513
NATIONAL APPLIC. NO.: WO 2003US15362 APPLIC. DATE: 20030513
LANGUAGE: English

...ABSTRACT: proximity-modulated signal generating system. The hybrid of the first and second targeting portions with the target polynucleotide comprises changed conformations in the probe that *activate* the proximity-modulated signal generating system. DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following: (1) an oligonucleotide probe-target polynucleotide hybrid; (2) determining...

... proximity-modulated signal generating system. The hybrid of the first and second targeting portions with the target polynucleotide comprises changed conformations in the probe that *activate* the proximity-modulated signal generating system. The proximity-modulated signal generating system comprises an energy transfer system. It also comprises an emitter and a quencher, or an emitter, a quencher and a harvester. It is *activated* by conformational changes in the probe induced by *hybridization* of the probe with the target molecule. The first and second targeting portions comprise segments that do not *hybridize* to each other. The first targeting portion comprises at least two internally complementary segments. It is a *hairpin* oligonucleotide. It comprises a first quencher and a first emitter in close spatial proximity to afford quenching of the first emitter by the first quencher...

... separated by the linker portion that is different from the first or second targeting portion, and form a fluorescent resonance energy transfer (FRET) pair. The *hairpin* oligonucleotide comprises a loop portion and two switch portions located at the ends of the *hairpin* oligonucleotide. The switch portions are complementary to each other and form a *hybridized* duplex sequence. The loop portion *hybridizes* to the target polynucleotide. The oligonucleotide probe is attached to a solid support. It further comprises a linker positioned between the first and second targeting portions. The linker is also positioned between the harvester and emitter. The linker comprises a sequence of nucleotides that does not *hybridize* to either the first or second targeting portion. The linker portion is a polymer. The harvester comprises tetramethylrhodamine, fluorescein, 4-(4-dimethylamino-phenyla zo)-benzoic acid...

... indacene (BODIPY) FL. The quencher comprises DABCYL or BlackHole (RTM) dye. The quenchers are the same or different chemical structure. When the oligonucleotide probe is *hybridized* to the target polynucleotide, the emitter and quencher are positioned so that the emitter is not quenched and the harvester and emitter are positioned so...

... oligonucleotide probe; (b) subjecting the probe to incident energy; and (c) detecting a signal generated by the probe. Step (a) is performed under conditions promoting *hybridization* of the target polynucleotide with the first and second targeting portions. Detecting a target polynucleotide comprises contacting the target polynucleotide with the oligonucleotide probe. The *hybridization* of the probe with the target polynucleotide results in the emitter and harvester being separated from each other by 0.1-2.0, 0.25...

4/3,K/14 (Item 2 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.

0323895 DBR Accession No.: 2003-25035 PATENT
New polo-like kinase 1 agent containing duplex RNAs antisense oligonucleotides and inhibitory peptides, useful for treating disorders with elevated PLK1 expression levels, such as proliferative diseases,

particularly cancer - small interfering RNA or antisense RNA transfer and expression in host cell for gene therapy

AUTHOR: STREBHARDT K; SPAENKUCH-SCHMITT B; YUAN J
PATENT ASSIGNEE: STREBHARDT K 2003
PATENT NUMBER: WO 200370283 PATENT DATE: 20030828 WPI ACCESSION NO.: 2003-697573 (200366)
PRIORITY APPLIC. NO.: EP 200225103 APPLIC. DATE: 20021108
NATIONAL APPLIC. NO.: WO 2003EP1809 APPLIC. DATE: 20030221
LANGUAGE: English

...ABSTRACT: genetic information under suitable conditions and in the presence of an RNA polymerase is transcribed into interfering RNA that is a siRNA, preferably a shRNA (*hairpin*) or a short antisense RNA. The RNA expression system is contained in a plasmid or viral vector. The genetic information comprises two complementary and inverted...

... systems. (I) further comprises peptide P1 and/or peptide P2. ACTIVITY - Cytostatic. 26 phosphorothioate antisense oligonucleotides (ASOs),each 20 nucleotides in length and predicted to *hybridize* with human PLK1 mRNA were tested to identify effective candidates capable of inhibiting PLK1 gene expression in human tumor cells. The results showed that the ...

...of the mRNA for a specific gene results in gradual downregulation of the protein and loss of function of that gene mostly due to the *activation* of RNase H, which leaves the mRNA at RNA/DNA duplex sites. ASOs, named P12 and P13, are efficient inhibitors for reducing PLK1 mRNA in...

4/3,K/15 (Item 3 from file: 357)

DIALOG(R)File 357:Derwent Biotech Res.

0317529 DBR Accession No.: 2003-18669 PATENT

Detecting a target double stranded nucleic acid sequence in a sample, using the probes having sequences homologous to adjacent portions of the target nucleic acid sequences - ds DNA detection using DNA probe pair

AUTHOR: ALBAGLI D; VANATTA R; WOOD M
PATENT ASSIGNEE: NAXCOR 2003
PATENT NUMBER: US 20030039961 PATENT DATE: 20030227 WPI ACCESSION NO.: 2003-492158 (200346)
PRIORITY APPLIC. NO.: US 757563 APPLIC. DATE: 20010109
NATIONAL APPLIC. NO.: US 757563 APPLIC. DATE: 20010109
LANGUAGE: English

...ABSTRACT: of (P) to (I), comprising combining the sample with (P) to produce an assay medium, where (P) which binds to (I) form the stem, and *activating* the *activatable* group, is new. DETAILED DESCRIPTION - M1 comprises detecting a target nucleic acid sequence in a sample, employing at least one pair of probes having sequences...

... to form a stem upon base pairing of the probes to the target nucleic acid sequence, at least one of the side chains having an *activatable* group, which upon *activation* during stem formation forms a covalent cross-link with the other side chain member of the stem, by combining the sample with at least one...

... pairing between the probes and the target nucleic acid to produce an assay medium, where probes binding to the target nucleic acid form the stem, *activating* the *activatable* group, where a covalent cross-link occurs between the side chain sequence in the sample. INDEPENDENT CLAIMS are also included for: (1) a kit comprising...

... to form a stem upon base pairing of the probes to the target nucleic acid sequence, at least one of the side chains having an *activatable* group, which upon *activation* during stem formation forms a covalent

cross-link with the other side chain member of the stem; (2) a nucleic acid compound comprising a nucleic...

... to form a stem upon base pairing of the probes to the target nucleic acid sequence, at least one of the side chains having an *activatable* group, which upon *activation* during stem formation forms a covalent cross-link with the other side chain member of the stem, where the method, sample and the probes are combined in an assay medium under base-pairing conditions, the *activatable* groups are *activated* resulting in cross-linked pairs of probes and the cross-linked pairs of probes are detected as indicative of the presence of the target sequence...

... base pairing conditions of the assay medium, and a control circuit responsive to the base pairing conditions of the medium and configured to actuate an *activator* for the *activatable* group at a predetermined assay medium condition, or a thermal cycler for modulating the temperature of the assay medium, a control circuit responsive to the temperature of the assay medium and configured to actuate an irradiation source for *activating* the *activatable* group when the temperature is below a first predetermined temperature, and an assay containment unit for holding the assay medium. BIOTECHNOLOGY - Preferred Method: The *activating* is photoactivating, and the target nucleic acid is double stranded and two different pairs of probes are used, where each pair is homologous to one...

... nucleotides between the sequences homologous to the pair of probes and each of the side chains of the stem comprise at least three nucleotides or *hybridizing* its analogs which form base pairs. The side chains have 3-8 nucleotides or *hybridizing* its analogs which base pair to form the stem. The photoactivatable group reacts with a nucleotide or its analog to form a covalent bond cross...
... directly linked to the side chain and the first nucleotide base pairing with a nucleotide of the other side chain member of the stem. The *hairpin* comprises a bulge comprising the photoactivatable group and one of the side chains comprises a terminal sequence complementary to the sequence homologous to the target...

...nucleotide base pairing with a nucleotide of the other side chain member of the stem. At least one of the side chains which comprises an *activatable* group forms a *hairpin* or stem and loop by one portion of the side chain binding to a different portion of the side chain or to the sequence of...

... a directly detectable label such as fluorophore. Preferred Device: The base pairing conditions of the assay medium is the temperature of the medium, and the *activatable* group is a photoactivatable group and the *activator* is an irradiation source. The control circuit comprises a thermistor for transducing the temperature of the assay medium into an electrical signal, and is configured...

4/3,K/16 (Item 4 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.

0307337 DBR Accession No.: 2003-09122 PATENT
Novel eukaryotic chromosome comprising one or many att sites which permits site-directed integration in the presence of lambda-integrase, useful for site-specific recombination-directed integration of DNA of interest - artificial chromosome-mediated gene transfer and expression in host cell for gene therapy
AUTHOR: PERKINS E; PEREZ C; LINDENBAUM M; GREENE A; LEUNG J; FLEMING E ; STEWART S; SHELLARD J
PATENT ASSIGNEE: CHROMOS MOLECULAR SYSTEMS INC 2002
PATENT NUMBER: WO 200297059 PATENT DATE: 20021205 WPI ACCESSION NO.: 2003-140461 (200313)

PRIORITY APPLIC. NO.: US 366891 APPLIC. DATE: 20020321
NATIONAL APPLIC. NO.: WO 2002US17452 APPLIC. DATE: 20020530
LANGUAGE: English

...ABSTRACT: or lox P sites. The first and/or second recombination site contains at least one mutation that removes one or more stop codons, or avoids *hairpin* formation. The first and/or second recombination site comprises at least a first nucleic acid sequence chosen from 16 sequences fully defined in the specification...
... selectable marker is an antibiotic resistance gene, and a detectable protein such as chromogenic, fluorescent or capable of being bound by an antibody and fluorescence *activated* cell sorting (FACS) sorted. Preferably, the selectable marker is green fluorescent protein (GFP), red fluorescent protein (RFP), blue fluorescent protein (BFP) or Escherichia coli histidinol...

... second recombination site. In (M3), the reporter is operatively linked to a promoter that controls expression of a gene in a signal transduction pathway, where *activation* or reduction in the signal indicates that the pathway is *activated* or down-regulated by the test compound. The reporter in the construct encodes drug resistance or a fluorescent protein. The ACes comprises several reporter-linked...to proliferate in the selective medium after cloning. No colonies were seen on the control plates after 37 days in selective medium. Fluorescent in situ *hybridization* (FISH) analysis was performed on the candidate clones to detect ACes formation. Metaphase spreads from the candidate clones were probed in multiple probe combinations. Candidate...

4/3,K/17 (Item 5 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.

0303226 DBR Accession No.: 2003-05011 PATENT
Synthesizing chemical compounds by hybridizing one or more templates which have associated reactive unit, with one or more transfer units having anti-codon and reactive unit, and performing reaction of reactive units - antisense DNA synthesis and DNA library construction for catalyst, drug or polymer development and gene therapy
AUTHOR: LIU D R; GARTNER Z J; KANAN M W
PATENT ASSIGNEE: HARVARD COLLEGE 2002
PATENT NUMBER: WO 200274929 PATENT DATE: 20020926 WPI ACCESSION NO.: 2002-740858 (200280)
PRIORITY APPLIC. NO.: US 101030 APPLIC. DATE: 20020319
NATIONAL APPLIC. NO.: WO 2002US8546 APPLIC. DATE: 20020319
LANGUAGE: English

...ABSTRACT: and contacting one or more transfer units having an anti-codon and reactive unit with the one or more templates under conditions to allow for *hybridization* of the one or more anti-codons to template, and reaction of the reactive units. DETAILED DESCRIPTION - INDEPENDENT CLAIMS are included for the following: (1...

... one or more nucleic acid templates, contacting one or more transfer units with the one or more nucleic acid template under conditions to allow for *hybridization* and reaction to form bonds between adjacent monomer units lined up along the template; and (4) a library (I) comprising one or more chemical compounds...

... are also disclosed. BIOTECHNOLOGY - Preferred Method: In M1, a portion of one or more chemical compounds contain an anti-codon comprising a nucleotide sequence which *hybridizes* with one or more nucleic acid templates. The chemical compound synthesized is a compound other than an nucleic acid or a nucleic acid analog. M1...

...shuffling). M3 further involves isolating the non-natural polymer, where

a portion of non-natural polymers contain an anti-codon comprising a nucleotide sequence which *hybridizes* with one or more nucleic acid templates. The nucleic acid template employed in the above mentioned methods is single- or double-stranded and is chosen...

... used in modifying a small molecule scaffold. USE - For synthesizing one or more chemical compounds which contain an anti-codon comprising a nucleotide sequence which *hybridizes* with one or more nucleic acid templates. M1 is useful for synthesizing a library of chemical compounds (all claimed). The method can be used to...

...enables the isolation of novel ligands or drugs with properties superior to those isolated by traditional rational design or combinatorial screening drug discovery methods. EXAMPLE - *Hairpin* (H) and end-of-helix (E) templates bearing electrophilic maleimide groups were used to support solution-phase DNA-templated synthesis. DNA templated reaction rates (kapp...products differ markedly from the structure of the natural. The ability of the DNA-templated synthesis to direct reactions that require a non-DNA-linked *activator*, catalyst or other reagent was tested.To test the ability of DNA-templated synthesis to mediate such reactions without requiring structural mimicry of the DNA ...

...EDC, and surprisingly insensitive to the steric encumbrance of the amine or carboxylate. Efficient DNA-templated amide formation was also mediated by the water-stable *activator* 4-(4,6-diemthoxy-1,3,5-trizin-2-yl)-4-methylmorpholinium chloride (DMT-MM) instead of EDC and sulfo-NHS. The efficiency and generality...

4/3,K/18 (Item 6 from file: 357)

0302118 DBR Accession No.: 2003-03903 PATENT

Amplifying specific nucleic acid molecules, useful for genotyping, allotyping, detecting genetic or infectious diseases, specific point mutations, or polymorphism, comprises providing a closed circular padlock probe molecule - DNA detection, DNA probe and DNA primer useful for genomic and disease diagnosis

AUTHOR: THOMAS D C
PATENT ASSIGNEE: VIRCO CENT VIROLOGICAL LAB IRELAND LTD 2002
PATENT NUMBER: WO 200268683 PATENT DATE: 20020906 WPI ACCESSION NO.: 2002-707011 (200276)
PRIORITY APPLIC. NO.: US 271433 APPLIC. DATE: 20010227
NATIONAL APPLIC. NO.: WO 2002EP2287 APPLIC. DATE: 20020227
LANGUAGE: English

...ABSTRACT: molecule, a forward primer, a reverse primer, dNTPs, and a first DNA polymerase to form a reaction mixture; (b) creating a multi-tailed complex; (c) *activating* a second DNA polymerase, which is thermostable; and (d) thermocycling the multi-tailed complex. INDEPENDENT CLAIMS are also included for the following: (1) a nucleic ...

... the reaction tube; (c) creating a closed circular padlock probe molecule; (d) creating a multi-tailed complex from the closed circular padlock probe molecule; (e) *activating* a second DNA polymerase, which is a thermostable DNA polymerase; and (f) thermocycling the multi-tailed complex; and (4) a padlock probe amplification primer comprises...

... region of the forward or reverse primer is a tailed primer molecule. At least one of the forward primer or reverse primer is: (a) a *hairpin* primer that has a loop region containing a restriction endonuclease cleavage site; or (b) detectably labeled that contains a molecular energy transfer mechanism. At least...

... first DNA polymerase; (b) creating a closed circular padlock probe

molecule; (c) creating a multi-tailed complex from the closed circular padlock probe molecule; (d) *activating* a second DNA polymerase; (e) thermocycling the multi-tailed complex with the second DNA polymerase; and (f) detecting the amplification product of the multi-tailed...

...forward primer, a reverse primer, dNTPs, and a first DNA polymerase; (b) creating a multi-tailed complex from the closed circular padlock probe molecule; (c) *activating* a second DNA polymerase; (d) thermocycling the multi-tailed complex with the second DNA polymerase; and (e) detecting the amplification product of the multi-tailed...

... acid molecules, a forward primer and a reverse primer; (d) creating a multi-tailed complex for each of the distinct target nucleic acid molecules; (e) *activating* a second DNA polymerase; (f) thermocycling at least two distinct multi-tailed complexes with the second DNA polymerase; and (g) detecting the amplification products of...

... complexes. At least one of the two closed circular nucleic acid molecules, where the 5' terminal region of the forward or reverse primer does not *hybridize* to the closed circular nucleic acid molecule. The ligase enzyme used in the closed tube nucleic acid molecule amplification method, is a thermolabile ligase enzyme...

4/3,K/19 (Item 7 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.

0299425 DBR Accession No.: 2003-01209 PATENT
A *hairpin* type ribozyme *activated* by the change in stem-loop three dimentional structure by *hybridization* with an oligonucleotide - vector-mediated gene transfer and expression in host cell for polymorphism detection in a gene
PATENT ASSIGNEE: DNA CHIP KENKYUSHO KK; HITACHI SOFTWARE ENG CO LTD 2002
PATENT NUMBER: JP 2002191368 PATENT DATE: 20020709 WPI ACCESSION NO.: 2002-630903 (200268)
PRIORITY APPLIC. NO.: JP 2000399155 APPLIC. DATE: 20001227
NATIONAL APPLIC. NO.: JP 2000399155 APPLIC. DATE: 20001227
LANGUAGE: Japanese

A *hairpin* type ribozyme *activated* by the change in stem-loop three dimentional structure by *hybridization* with an oligonucleotide - vector-mediated gene transfer and expression in host cell for polymorphism detection in a gene
ABSTRACT: DERWENT ABSTRACT: NOVELTY - A *hairpin* type ribozyme (I) *activated* by the change in stem-loop three dimentional structure by *hybridization* with an oligonucleotide, is new. DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for: (1) a deoxyribonucleic acid (DNA) (II) encoding a ribonucleotide constituting (I); (2) a recombinant vector (III) containing (II); (3) a host cell in which (III) is introduced; (4) *activating* a *hairpin* type ribozyme by changing the stem-loop three dimentional structure by *hybridization* of an oligonucleotide with an inactivated ribozyme; (5) detecting a target base sequence using (I); (6) a kit for detecting a target base sequence in...

4/3,K/20 (Item 8 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.

0287802 DBR Accession No.: 2002-09649 PATENT
Probes for detecting target nucleotide sequence in sample, has sequence that forms hairpin structure having a double-stranded segment and single-stranded loop collectively forming region complementary to target sequence - oligonucleotide DNA probe, RNA probe, peptide nucleic acid probe for detecting target sequence in a sample and for

transcription and/or DNA amplification of probe sequence

AUTHOR: DATTAGUPTA N
PATENT ASSIGNEE: APPLIED GENE TECHNOLOGIES INC 2002
PATENT NUMBER: WO 200206531 PATENT DATE: 20020124 WPI ACCESSION NO.: 2002-171819 (200222)
PRIORITY APPLIC. NO.: US 823647 APPLIC. DATE: 20010330
NATIONAL APPLIC. NO.: WO 2001US22166 APPLIC. DATE: 20010712
LANGUAGE: English

ABSTRACT: DERWENT ABSTRACT: NOVELTY - An oligonucleotide probe (I) comprising a nucleotide sequence (S1) that forms a *hairpin* structure having a double stranded segment (DSS) and a single stranded loop (SSL), where (S1) is located with DSS only, or a portion of (S1...

... within SSL, collectively forming a region that is complementary to a target nucleotide sequence (TS), is new. DETAILED DESCRIPTION - (I) comprises (S1) that forms a *hairpin* structure having DSS and SSL, where SSL contains at least 3 nucleotides and the DSS is formed between two complementary nucleotide sequences under suitable conditions...

... perfectly matched nucleotide sequences and at least a portion of the nucleotide sequences located solely within the DSS is complementary to a TS to be *hybridized* with; or (b) a portion of the nucleotide sequences located within DSS and a portion the nucleotide sequences located within the single stranded loop collectively form a region that is complementary to a TS to be *hybridized* with. An INDEPENDENT CLAIM is also included for: (1) an array (II) of oligonucleotide probes immobilized on a support for *hybridization* analysis comprising a solid support having several immobilized probes containing at least one of (I); (2) detecting (M1) a target nucleotide sequence (TS) in a...

...sequence in TS, where SSL of probe comprises 3-10 or 15 nucleotides. (I) further comprises: (a) an element, preferably a crosslinking agent that is *activated* by chemical or photoactive treatment, which is a furocoumarin, a macromolecule having multiple ligand binding sites which is a component of biotin-avidin binding system...
... preferably biosample containing or suspected of containing TS, at a temperature of 4-90degreesC, for 1-60 minutes and under conditions that favor intermolecular (ITER) *hybridization* between (I) and TS over intramolecular (ITRA) *hybridization* of the probe itself and assessing the intermolecular hybrid form, where the conditions that favor *hybridization* is achieved by controlling compositions of (I) and TS so that Tm of the ITER hybrid is higher than Tm of ITRA hybrid preferably ITER...

... enzymatic, radioactive, fluorescent, luminescent and fluorescence resonance energy transfer (FRET) label and ITER is assessed by addition of a detectably labeled secondary probe that specifically *hybridizes* with a portion of ITER and detection of secondary ITER hybrid formed between secondary probe and original ITER, indicating the presence of TS in the...

... ITRA are crosslinked after the formation of ITER but before addition of secondary probe where crosslinking is effected via addition of an agent subsequent to *hybridization* of the original probe with TS. The *hairpin* structure in (I) is formed between a DNA strand that contains methylphosphonates and RNA strand that is complementary to TS. (M2) comprises contacting (I) with...
... were extended at the 3' end up to 30 extra nucleotide residues, first 9 residues were made of dT to function as spacer for the *hairpin* structure; the rest (21 residues) was complementary to the probe sequence and sequentially organized as 7 deoxy-6 ribo-8 deoxy residues; the probe sequence had methylphosphonates complementary to the ribose residues in the chain. This prevented RNase H digestion of the unhybridized *hairpin* probe. This also reduced the Tm of the probe compared to an RNA-DNA hybrid formed with a target. For example, the probe 5'-CATCCGTAACTAcatcttcca...

... method and genomic HPV DNA was purified from samples by proteinase K digestion and ethanol precipitation as described in Gravitt at el (supra). The immobilized *hairpin* probe containing strip was *hybridized* with the sample DNA at 53degreesC overnight in a buffer containing 0.72 M NaCl, 40 mM NaH2PO4 and 4 mM EDTA (pH 7.7). After *hybridization*, the strip was twice with the *hybridization* buffer at 47degreesC and RNase H buffer once. The strip containing the hybrid was then treated with RNase H to digest the part of the *hybridized* probe with RNA-DNA hybrid structure. This was carried out by using 1 unit of RNase H from Sigma Chemical Co. per ml of the...

... hybrid in the digestion buffer containing the enzyme for 1 hour at 37degreesC, hybrids containing RNA-DNA structure were digested and under these conditions the *hairpin* intra-molecular hybrid was not disturbed. After enzyme digestion, the strip was washed with *hybridization* buffer and a secondary *hybridization* was carried out with biotin labeled probes. The labeled probes were equal weight by weight mixtures of oligonucleotides complementary to the immobilized probe portions which become single stranded after *hybridization* and digestion. After the second *hybridization* and washing, biotin in the hybrid was detected by using a streptavidin-horseradish peroxidase conjugate chemiluminescence. This was carried out by soaking the array in...

...was recorded on a POLAROID film. Biotin sites appeared as white spots on the film. The sites where biotin was detected were the site of *hybridization* of the target sample and the corresponding sequence was the sequence of the target present in the sample. (72 pages)

4/3,K/21 (Item 1 from file: 370)

00504539 (USE 9 FOR FULLTEXT)

Hyaluronan Synthase of Chlorella Virus PBCV-1

DeAngelis, Paul L.; Jing, Wei; Graves, Michael V.; Burbank, Dwight E.; Van Etten, James L.
P. L. DeAngelis and W. Jing, Department of Biochemistry and Molecular Biology, University of Oklahoma Health Sciences Center, 940 Stanton L. Young Boulevard, Oklahoma City, OK 73104, USA. ; M. V. Graves, D. E. Burbank, J. L. Van Etten, Department of Plant Pathology, University of Nebraska, Lincoln, NE 68583-0722, USA.

Science Vol. 278 5344 pp. 1800
Publication Date: 12-05-1997 (971205) Publication Year: 1997
Document Type: Journal ISSN: 0036-8075
Language: English
Section Heading: Reports
Word Count: 2049

(THIS IS THE FULLTEXT)

...Text: HA synthases (HASs) are integral membrane proteins that polymerize the HA molecule using *activated* uridine diphosphate (UDP)-sugar nucleotides as substrates. Amino acid sequences for some HASs have been deduced from gene sequencing (B8) ; their sizes range from 419...

...component located inside the outer glycoprotein capsid (B10) . The PBCV-1 genome is a linear, nonpermuted 330-kb double-stranded DNA molecule with covalently closed *hairpin* ends (B11...were tested for the presence of an A98R-like gene and for the ability to direct production of HA polysaccharide in Chlorella NC64A. Dot-blot *hybridization* analyses of the individual viral genomes with the PBCV-1 A98R probe indicated that 19 isolates (58%) had a similar gene; the algal host DNA...

4/3,K/22 (Item 2 from file: 370)
DIALOG(R)File 370:Science

00500737 (USE 9 FOR FULLTEXT)
A Cellular Homolog of Hepatitis Delta Antigen: Implications for Viral Replication and Evolution
Brazas, Robert; Ganem, Don
R. Brazas, Departments of Microbiology and Medicine, University of California, San Francisco, CA 94143, USA. ; D. Ganem, Howard Hughes Medical Institute and Departments of Microbiology and Medicine, University of California, San Francisco, CA 94143, USA.
Science Vol. 274 5284 pp. 90
Publication Date: 10-04-1996 (961004) Publication Year: 1996
Document Type: Journal ISSN: 0036-8075
Language: English
Section Heading: Reports
Word Count: 3032

(THIS IS THE FULLTEXT)

...Text: the DNA binding domain of Gal4p and HDAg were transformed with a library of human cDNAs that were fused to the sequence encoding the Gal4p *activation* domain (B12) . Of ~2 x 10.sup(6) independent transformants, 19 were selected on the basis of their ability to *activate* transcription of a HIS3 reporter gene under the control of multiple Gal4p binding sites. From these 19 original His.sup(+) transformants, 12, each of which...this template, would result in the capture of DIPA sequences. We propose that, after copying to the 5 (prime) end of the DIPA template, a *hairpin* formed at the 3 (prime) end of the newly synthesized RNA would allow synthesis to continue to complete the newly formed HDV genome. Further evolution...

...was subsequently detected with alkaline phosphatase-conjugated antibodies to digoxigenin (B13) . (B) Expression of DIPA in human tissues. A multiple-tissue Northern blot was also *hybridized* with the DIPA-specific riboprobe (top row) and, subsequently, with an actin-specific riboprobe (bottom row). The positions of the 1.1-kb DIPA mRNA...

4/3,K/23 (Item 3 from file: 370)
DIALOG(R)File 370:Science

00500711 (USE 9 FOR FULLTEXT)
Highly Diverged U4 and U6 Small Nuclear RNAs Required for Splicing Rare AT-AC Introns
Tarn, Woan-Yuh; Steitz, Joan A.
Department of Molecular Biophysics and Biochemistry, Yale University School of Medicine, Howard Hughes Medical Institute, New Haven, CT 06536-0812, USA.
Science Vol. 273 5283 pp. 1824
Publication Date: 9-27-1996 (960927) Publication Year: 1996
Document Type: Journal ISSN: 0036-8075
Language: English
Section Heading: Research Articles
Word Count: 6743

(THIS IS THE FULLTEXT)

...Text: pre-mRNA on a nondenaturing polyacrylamide gel and then performed Northern blot analyses (B5) . Parallel splicing reactions containing the adenovirus pre-mRNA served as controls. *Hybridization* with a U4atac probe yielded a signal in complex B at 40 minutes and thereafter, but not in any of the other splicing complexes (Fig...
...As expected, both complexes B and C, but not complexes A-1 and A-2, were detected when the blot was *hybridized* with a U6atac probe (Fig. 3, lanes

20 through 25). The U6atac antisense probe also *hybridized* to a fast-migrating complex representing a free U6atac snRNP particle. This is consistent with the observation from glycerol gradient analyses that a portion of...

...the U4atac nor U6atac probe reacted with splicing complexes assembled on the adenovirus pre-mRNA (lanes 3 and 4 and 15 and 16), which strongly *hybridized* with antisense RNA probes to U4 and U6 (B5) . The association of U4atac and U6atac RNAs with the P120 pre-mRNA during splicing was confirmed...365-nm light in the presence of AMT psoralen. RNAs extracted from these samples were fractionated on a gel and identified by Northern blot analysis. *Hybridization* with a U12 probe detected several slowly migrating bands whose RNA content was determined by RNase H digestion directed by oligonucleotides complementary to snRNAs or...Fig. 6B, upper). These structures are comparable with those in the major spliceosome and predict that unwinding of U4atac from U6atac will be required for *activation* of the AT-AC spliceosome. This scenario is consistent with the lack of U4atac in complex C (Fig. 3) and the observation that the U4...U6 intramolecular interaction that, in conjunction with U2-U6 helix Ia and helix III, yields a structure more closely resembling the catalytic domain of the *hairpin* ribozyme. Although a potential U2-U6 helix III structure had been earlier noted in several species (B39) , it may not contribute significantly to splicing in...61 through 79 of U6atac (lane 5). RNAs were fractionated on a 6 percent polyacrylamide gel and transferred onto a nylon membrane. The blot was *hybridized* with an anti-U6atac riboprobe. The procedures for psoralen crosslinking, RNase H digestion, and Northern blot analysis were essentially according to (B5) . U4atac and U6atac...

...4) of 75 nM adenovirus pre-mRNA. Complexes were separated on a native gel and transferred onto a nylon membrane (B5) . The blot was previously *hybridized* with several probes including anti-U12 (lanes 1 and 2) (B5) . *Hybridization* with antisense U4atac and U6atac riboprobes was carried out according to (B5) . The identities of P120 complexes as determined previously (B5) are indicated at the...lane 6 except that ATP was omitted (lane 8). Recovered RNAs were fractionated on a 6 percent polyacrylamide gel and transferred onto a nylon membrane. *Hybridization* with an anti-U12 riboprobe was carried out as described previously (B5) . The identi-ties of crosslinked RNAs were determined in (B). The asterisk represents...

4/3,K/24 (Item 4 from file: 370)

00500668 (USE 9 FOR FULLTEXT)
Correction of the Mutation Responsible for Sickle Cell Anemia by an RNA-DNA Oligonucleotide
Cole-Strauss, Allyson; Yoon, Kyonggeun; Xiang, Yufei; Byrne, Bruce C.; Rice, Michael C.; Gryn, Jeff; Holloman, William K.; Kmiec, Eric B.
A. Cole-Strauss, K. Yoon, Y. Xiang, M. C. Rice, E. B. Kmiec, Department of Pharmacology, Kimmel Cancer Center, Thomas Jefferson University, 233 South 10th Street, Philadelphia, PA 19107, USA. ; B. C. Byrne and J. Gryn, Division of Hematology-Oncology, Department of Medicine, Cooper Hospital University Medical Center, Camden, NJ 08103, USA. ; W. K. Holloman, Department of Microbiology, Cornell University School of Medicine, 1300 York Avenue, New York, NY, USA.
Science Vol. 273 5280 pp. 1386
Publication Date: 9-06-1996 (960906) Publication Year: 1996
Document Type: Journal ISSN: 0036-8075
Language: English
Section Heading: Reports
Word Count: 2055

(THIS IS THE FULLTEXT)
...Text: The design of this molecule was prompted by the discovery that RNA-DNA hybrids were highly active in homologous pairing reactions in vitro and that *hairpin* caps at the ends of hybrid molecules were no impediment

to pairing (B5) . These observations suggested a strategy for targeted correction in which a short, double-stranded oligonucleotide vector is *activated* for recombination by incorporating RNA residues and protected from exonucleolytic degradation by capping both ends. The 2 (prime) -O-methyl modification of ribose of the...Figure Removed

Figure F2
Caption: Southern *hybridization* analysis of DNA from SC1-treated cells. Genomic DNA from (beta) .sup(A) control cells and (beta) .sup(S) cells transfected with SC1 was cut with Bsu 36I and analyzed by Southern *hybridization*. Globin DNA from (beta) .sup(A) and (beta) .sup(S) migrates as 1.2-and 1.4-kbp fragments, respectively, indicated to the right ...

4/3,K/25 (Item 5 from file: 370)
DIALOG(R)File 370:Science

00500599 (USE 9 FOR FULLTEXT)
Genome Sequence of a Human Tumorigenic Poxvirus: Prediction of Specific Host Response-Evasion Genes
Senkevich, Tatiana G.; Bugert, Joachim J.; Sisler, Jerry R.; Koonin, Eugene V.; Darai, Gholamreza; Moss, Bernard
T. G. Senkevich, J. J. Bugert, J. R. Sisler, B. Moss, Laboratory of Viral Diseases, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, MD 20892-0455, USA. ; E. V. Koonin, National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, Bethesda, MD 20892, USA. ; G. Darai, Institut fuer Medizinische Virologie, Universitaet Heidelberg, 69120 Heidelberg, Germany.
Science Vol. 273 5276 pp. 813
Publication Date: 8-09-1996 (960809) Publication Year: 1996
Document Type: Journal ISSN: 0036-8075
Language: English
Section Heading: Reports
Word Count: 2829

(THIS IS THE FULLTEXT)
...Text: to VAR or VV, as revealed by a nearly twofold higher GC content (63% in MCV, 34% in VAR and VV), lack of DNA cross-*hybridization* or immunological cross-reactivity, and sequence differences in the short segments of MCV DNA that have heretofore been analyzed (B4...

...100,000 nucleotides. The 190,289-base pair (bp) sequence of MCV DNA, comprising the entire genome with the exception of the covalently closed terminal *hairpin* loops (B7) (B8) , was deposited in GenBank (accession number U60315). The MCV DNA has a GC content of 63.3%, resulting in a paucity of...MCV protein is predicted to retain the disulfide bonding pattern and the general structure of chemokines, the NH.inf(2)-terminal region implicated in monocyte *activation* (B21) is deleted. Truncated analogs of CC chemokines have been shown to bind their receptors but have no activity (B21) . Therefore, the MCV protein is...

4/3,K/26 (Item 1 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)

137075225 CA: 137(6)75225h PATENT
Hairpin ribozymes activatable by oligonucleotide hybridization causing stem loop conformation change
INVENTOR(AUTHOR): Komatsu, Yasuo; Otsuka, Eiko
LOCATION: Japan,
ASSIGNEE: D.N.H. Chip Kenkyusho K. K.; Hitachi Software Engineering Co., Ltd.
PATENT: Japan Kokai Tokkyo Koho ; JP 2002191368 A2 DATE: 20020709

APPLICATION: JP 2000399155 (20001227)
PAGES: 23 pp. CODEN: JKXXAF LANGUAGE: Japanese CLASS: C12N-015/09A; A61K-031/713B; A61P-031/18B; A61P-035/00B; C12M-001/00B; C12N-001/15B; C12N-001/19B; C12N-001/21B; C12N-005/10B; C12N-009/00B; C12Q-001/68B

4/3,K/27 (Item 2 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)

113074246 CA: 113(9)74246h PATENT
Nucleic acid hybridization assay and kit using a probe with a target-activated sequence for initiating primer extension or transcription
INVENTOR(AUTHOR): Chu, Barbara Chen Fei; Joyce, Gerald Francis; Orgel, Leslie Eleazer
LOCATION: USA
ASSIGNEE: Salk Institute for Biological Studies
PATENT: PCT International ; WO 9003445 A1 DATE: 900405
APPLICATION: WO 89US4206 (890928) *US 252093 (880930)
PAGES: 44 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: C12Q-001/68A; C07H-021/00B DESIGNATED COUNTRIES: JP DESIGNATED REGIONAL: AT; BE; CH; DE ; FR; GB; IT; LU; NL; SE

4/3,K/28 (Item 1 from file: 35)
DIALOG(R)File 35:Dissertation Abs Online

01623083 ORDER NO: AAD98-18169
"CAGED" DNA (CAGED DNA, NITROBENZYL, PHOTOCLEAVABLE, OLIGONUCLEOTIDES)
Author: ORDOUKHANIAN, PHILLIP TODD
Degree: PH.D.
Year: 1997
Corporate Source/Institution: WASHINGTON UNIVERSITY (0252)
Source: VOLUME 58/12-B OF DISSERTATION ABSTRACTS INTERNATIONAL. PAGE 6557. 146 PAGES

...ability to phototrigger single- and double-strand breaks in nucleic acids can be envisioned to be useful for a variety of applications, such as, the *activation* (or deactivation) of nucleic acid-based probes and drugs such as antisense oligonucleotides and ribozymes. With such applications in mind, we have designed a photochemically...

...and shown to result in DNA strand cleavage upon irradiation with wavelengths $>$350 nm. The building block was incorporated in the stem portion of a *hairpin* oligonucleotide and used as a way of phototriggering the release of a *hybridization* probe.

The photocleavable building block was also designed to produce one of the major types of strand breaks induced by ionizing radiation for use in ...
?

File 5:Biosis Previews(R) 1969-2004/Feb W3
(c) 2004 BIOSIS
File 6:NTIS 1964-2004/Feb W4
(c) 2004 NTIS, Intl Cpyrght All Rights Res
File 8:Ei Compendex(R) 1970-2004/Feb W2
(c) 2004 Elsevier Eng. Info. Inc.
File 34:SciSearch(R) Cited Ref Sci 1990-2004/Feb W2
(c) 2004 Inst for Sci Info
File 65:Inside Conferences 1993-2004/Feb W3
(c) 2004 BLDSC all rts. reserv.
File 71:ELSEVIER BIOBASE 1994-2004/Feb W2
(c) 2004 Elsevier Science B.V.
File 73:EMBASE 1974-2004/Feb W3
(c) 2004 Elsevier Science B.V.
File 94:JICST-EPlus 1985-2004/Feb W2
(c)2004 Japan Science and Tech Corp(JST)
File 98:General Sci Abs/Full-Text 1984-2004/Jan
(c) 2004 The HW Wilson Co.
File 99:Wilson Appl. Sci & Tech Abs 1983-2004/Jan
(c) 2004 The HW Wilson Co.
File 135:NewsRx Weekly Reports 1995-2004/Feb W3
(c) 2004 NewsRx
File 143:Biol. & Agric. Index 1983-2004/Jan
(c) 2004 The HW Wilson Co
File 144:Pascal 1973-2004/Feb W2
(c) 2004 INIST/CNRS
File 155:MEDLINE(R) 1966-2004/Feb W3
(c) format only 2004 The Dialog Corp.
File 172:EMBASE Alert 2004/Feb W2
(c) 2004 Elsevier Science B.V.
File 266:FEDRIP 2004/Jan
Comp & dist by NTIS, Intl Copyright All Rights Res
File 315:ChemEng & Biotec Abs 1970-2004/Jan
(c) 2004 DECHEMA
File 357:Derwent Biotech Res. _1982-2004/Feb W4
(c) 2004 Thomson Derwent & ISI
File 358:Current BioTech Abs 1983-2004/Jan
(c) 2004 DECHEMA
File 369:New Scientist 1994-2004/Feb W3
(c) 2004 Reed Business Information Ltd.
File 370:Science 1996-1999/Jul W3
(c) 1999 AAAS
File 399:CA SEARCH(R) 1967-2004/UD=14008
(c) 2004 American Chemical Society
File 434:SciSearch(R) Cited Ref Sci 1974-1989/Dec
(c) 1998 Inst for Sci Info
File 40:Enviroline(R) 1975-2004/Dec
File 50:CAB Abstracts 1972-2004/Jan
(c) 2004 CAB International
File 103:Energy SciTec 1974-2004/Feb B1
(c) 2004 Contains copyrighted material
File 156:ToxFile 1965-2004/Feb W3
(c) format only 2004 The Dialog Corporation
File 162:Global Health 1983-2004/Jan
(c) 2004 CAB International
File 305:Analytical Abstracts 1980-2004/Jan W2
(c) 2004 Royal Soc Chemistry
File 35:Dissertation Abs Online 1861-2004/Jan
(c) 2004 ProQuest Info&Learning
File 48:SPORTDiscus 1962-2004/Feb
(c) 2004 Sport Information Resource Centre
File 91:MANTIS(TM) 1880-2003/Feb
2001 (c) Action Potential
File 149:TGG Health&Wellness DB(SM) 1976-2004/Feb W2
(c) 2004 The Gale Group
File 159:Cancerlit 1975-2002/Oct
(c) format only 2002 Dialog Corporation

File 164:Allied & Complementary Medicine 1984-2004/Feb
(c) 2004 BLHCIS
File 444:New England Journal of Med. 1985-2004/Feb W4
(c) 2004 Mass. Med. Soc.
File 467:ExtraMED(tm) 2000/Dec
(c) 2001 Informania Ltd.

Set	Items	Description
S1	68	HAIRPIN (S) CIS (S) ACTIVAT?
S2	7	S1 (S) HYBRIDIZ?
S3	3	RD (unique items)
S4	14	S1 AND OLIGONUCLEOTIDE?
S5	6	RD (unique items)

>>>KWIC option is not available in file(s): 399

5/3,K/1 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0011835317 BIOSIS NO.: 199900094977
Dual blockade of cyclic AMP response element- (CRE) and AP-1-directed transcription by CRE-transcription factor decoy *oligonucleotide*. Gene-specific inhibition of tumor growth
AUTHOR: Park Yun Gyu; Nesterova Maria; Agrawal Sudhir; Cho-Chung Yoon S (Reprint)
AUTHOR ADDRESS: National Institutes Health, NCI, Build. 10, Room 5B05, Bethesda, MD 20892-1750, USA**USA
JOURNAL: Journal of Biological Chemistry 274 (3): p1573-1580 Jan. 15, 1999
1999
MEDIUM: print
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

Dual blockade of cyclic AMP response element- (CRE) and AP-1-directed transcription by CRE-transcription factor decoy *oligonucleotide*. Gene-specific inhibition of tumor growth

ABSTRACT: Alteration of gene transcription by inhibition of specific transcriptional regulatory proteins has important therapeutic potential. Synthetic double-stranded phosphorothioate *oligonucleotides* with high affinity for a target transcription factor can be introduced into cells as decoy *cis*-elements to bind the factors and alter gene expression. The CRE (cyclic AMP response element)transcription factor complex is a pleiotropic *activator* that participates in the induction of a wide variety of cellular and viral genes. Because the CRE *cis*-element, TGACGTCA, is palindromic, a synthetic single-stranded *oligonucleotide* composed of the CPE sequence self-hybridizes to form a duplex/*hairpin*. Herein we report that the CRE-palindromic *oligonucleotide* can penetrate into cells, compete with CRE enhancers for binding transcription factors, and specifically interfere with CRE- and AP-1-directed transcription in vivo. These *oligonucleotides* restrained tumor cell proliferation, without affecting the growth of noncancerous cells. This decoy *oligonucleotide* approach offers great promise as a tool for defining cellular regulatory processes and treating cancer and other diseases.
DESCRIPTORS:
CHEMICALS & BIOCHEMICALS: ...CRE-transcription factor decoy *oligonucleotide*

5/3,K/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0007689391 BIOSIS NO.: 199191072282
ACTION OF AN RNA SITE AT A DISTANCE ROLE OF THE NUT GENETIC SIGNAL IN

TRANSCRIPTION ANTITERMINATION BY PHAGE-LAMBDA N GENE PRODUCT

AUTHOR: WHALEN W A (Reprint); DAS A
AUTHOR ADDRESS: DEP MICROBIOL L2034 UNIV CONN HEALTH CENTER, 263 FARMINGTON AVE, FARMINGTON, CONN 06030, USA**USA
JOURNAL: New Biologist 2 (11): p975-991 1990
ISSN: 1043-4674
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The N gene product of Escherichia coli phage .lambda. is a transcriptional *activator* that captures the host RNA polymerase and modifies it to a termination-resistant form, permitting gene expression in two large polycistronic operons of the phage...

...in vitro requires at least one host factor called NusA, which directly binds the N protein as well as RNA polymerase, and also a transcribed *cis*-acting site known as nut, within which lies the hypothesized N-recognition signal, boxB. BoxB is an interrupted palindrome capable of forming a *hairpin* in the mRNA. Inhibition studies with complementary DNA *oligonucleotides* provide evidence for a direct role of the boxB *hairpin* in antitermination. Kinetic studies of transcript elongation reveal that the boxB *hairpin* does not induce an appreciable pause to hold polymerase captive for engagement by N and NusA. Moreover, the efficiency of antitermination remains virtually the same...

...amount of time and distance, and the nut site DNA becomes dispensable for this modification. These results lead to the hypothesis that the boxB RNA *hairpin* acts in a manner analogous to the DNA enhancers, binding N and mediating a productive polymerase-NusA-N interaction by mRNA looping.

5/3,K/3 (Item 1 from file: 71)

01101821 1999029464

Dual blockade of cyclic AMP response element- (CRE) and AP-1-directed transcription by CRE-transcription factor decoy *oligonucleotide*: Gene-specific inhibition of tumor growth

Yun Gyu Park; Nesterova M.; Agrawal S.; Cho-Chung Y.S.
ADDRESS: Y.S. Cho-Chung, National Institutes of Health, NCI, Bldg. 10, Bethesda, MD 20892-1750, United States
EMAIL: chochung@helix.nih.gov
Journal: Journal of Biological Chemistry, 274/3 (1573-1580), 1999, United States
PUBLICATION DATE: January 15, 1999
CODEN: JBCHA
ISSN: 0021-9258
DOCUMENT TYPE: Article
LANGUAGES: English SUMMARY LANGUAGES: English
NO. OF REFERENCES: 33

Dual blockade of cyclic AMP response element- (CRE) and AP-1-directed transcription by CRE-transcription factor decoy *oligonucleotide*: Gene-specific inhibition of tumor growth

Alteration of gene transcription by inhibition of specific transcriptional regulatory proteins has important therapeutic potential. Synthetic double-stranded phosphorothioate *oligonucleotides* with high affinity for a target transcription factor can be introduced into cells as decoy *cis* -elements to bind the factors and alter gene expression. The CRE (cyclic AMP response element)transcription factor complex is a pleiotropic *activator* that participates in the induction of a wide variety of cellular and viral genes. Because the CRE *cis*-element, TGACGTCA, is palindromic, a synthetic single-stranded *oligonucleotide* composed of the CRE sequence self- hybridizes to form a duplex/*hairpin*. Herein we report that the CRE- palindromic *oligonucleotide* can penetrate into cells,

compete with CRE enhancers for binding transcription factors, and specifically interfere with CRE- and AP-1-directed transcription in vivo. These *oligonucleotides* restrained tumor cell proliferation, without affecting the growth of noncancerous cells. This decoy *oligonucleotide* approach offers great promise as a tool for defining cellular regulatory processes and treating cancer and other diseases.

CLASSIFICATION CODE AND DESCRIPTION:
...*Oligonucleotide* synthesis and applications (antisense)
84.5.13.2 - GENETICS AND MOLECULAR BIOLOGY

5/3,K/4 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08911135 PMID: 1645778
Mutational analysis of the equine infectious anemia virus Tat-responsive element.
Carvalho M; Derse D
Laboratory of Viral Carcinogenesis, National Cancer Institute, Frederick, Maryland 21702-1201.
Journal of virology (UNITED STATES) Jul 1991, 65 (7) p3468-74, ISSN 0022-538X Journal Code: 0113724
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

M ~ QR355. J65

... the viral long terminal repeat. Premature termination of primer elongation at the predicted double-stranded RNA region was frequently observed and suggests that the inferred *hairpin* structure exists under these conditions. We have functionally characterized EIAV TAR by site-directed mutagenesis and transient gene expression analysis. It is demonstrated here that...

... element is essential for Tat action. Mutations that disrupted base pairing abolished TAR function, and compensatory mutations that restored the stem structure resulted in Tat *activation*. The TAR loop appears to be closed by two U.G base pairs that are likely to provide a unique structural motif recognized by the...

... the EIAV loop sequence decreased TAR function. All nucleotide substitutions of the cytidine at position +14 increased EIAV Tat responsiveness; however, its deletion abolished trans *activation*. Our results lead us to propose that the EIAV and HIV-1 Tat systems employ closely related *cis*- and trans-acting components that probably act by the same mechanism.
; Base Sequence; DNA Mutational Analysis; Hydrogen Bonding; Molecular Sequence Data; Nucleic Acid Conformation; *Oligonucleotides*--chemistry--CH ; RNA, Viral--genetics--GE; RNA, Viral--ultrastructure--UL; Repetitive Sequences, Nucleic Acid
Chemical Name: Gene Products, tat; *Oligonucleotides*; RNA, Viral

5/3,K/5 (Item 1 from file: 266)
DIALOG(R)File 266:FEDRIP

00315804
IDENTIFYING NO.: 1Z01BC10268-03 AGENCY CODE: CRISP
CRE-PALINDROMIC *OLIGONUCLEOTIDE* AS A TRANSCRIPTION FACTOR DECOY AND AN INHIBITOR
PRINCIPAL INVESTIGATOR: CHO CHUNG, YOON
SPONSORING ORG.: DIVISION OF BASIC SCIENCES - NCI
FY : 1999

CRE-PALINDROMIC *OLIGONUCLEOTIDE* AS A TRANSCRIPTION FACTOR DECOY AND AN INHIBITOR

SUMMARY: Synthetic double-stranded DNA with high affinity for a target transcription factor can be introduced into target cells as decoy *cis*-elements to bind the factor and alter gene transcription. The CRE (cyclic AMP response element)-transcription factor complex is a pleiotropic *activator* that participates in the induction of a wide variety of cellular and viral genes. Because the CRE *cis* -element TGACGTCA is palindromic, a synthetic single stranded *oligonucleotide* composed of the CRE sequence, which will self-hybridize to form either a duplex or *hairpin* , when introduced into a cell, can act as a decoy for the transcription factor. We have investigated the CRE-palindromic and -*hairpin* forming *oligonucleotides* as transcription factor decoys and the biological effects thereof. Herein we report that the CRE- palindromic *oligonucleotide* penetrated into cells, competed with CRE enhancers for binding transcription factors, and specifically interfered with CRE- and Ap-1-directed transcription in vivo. The 24 mer CRE palindrome *oligonucleotide* produced potent growth inhibition in a variety of cancer cells including breast, prostate, lung, ovarian, colon, and epidermoid carcinomas, and multidrug-resistant cancer cell lines...

... IC50, 100-200 nM). In contrast, the growth of normal human mammary epithelial cell and lung epithelial cell lines was not affected by the CRE *oligonucleotide* . Treatment of nude mice bearing HCT-15 MDR colon carcinoma with 24 mer CRE *oligonucleotide* (0.1 mg/0.1 ml saline/mouse ip, 5x/week for 4 weeks) resulted in >85% inhibition of tumor growth. The CRE-*oligonucleotide* -induced growth inhibition accompanied changes in cell morphology and the appearance of apoptotic nuclei. By comparison, two base-mismatched control *oligonucleotide* or a palindromic *oligonucleotide* containing no CRE sequence had no effect on either CRE-directed transcription or cell growth. The mechanism by which the blockade of CRE-gene transcription...

... this technology offers great promise as a tool for defining cellular regulatory processes and treating diseased conditions. - Cancer, Transcription, cyclic AMP response element, growth arrest, *oligonucleotide*, transcription factor-decoy, AP-1,

DESCRIPTORS: athymic mouse; cell growth regulation; pleiotropism; genetic regulatory element; genetic transcription; transcription factor; gene induction /repression; growth inhibitor; neoplastic growth; *oligonucleotide*; DNA binding protein; cyclic AMP

5/3,K/6 (Item 1 from file: 159)

01846784 PMID: 90666776

CHARACTERIZATION OF THE PROMOTER IN A HUMAN B19 PARVOVIRUS.

Blundell
Univ. of British Columbia, Canada

Diss Abstr Int [B] 1990, 50 (12), ISSN 0419-4217
Document Type: THESIS
Languages: ENGLISH
Main Citation Owner: NOTNLM
Record type: Completed

... that the termini may be imperfect inverted terminal repeats. The additional sequence present on the right-hand terminus of B19-Wi supported that supposition. The *hairpin* termini of the B19 genome were of the same type as those found in adeno-associated parvoviruses, and suggested B19 may be more closely related...

...two or more active promoters. A series of ordered deletions, prepared in the region upstream of the initiation site of the promoter, indicated that multiple *cis*-*activating* motifs were required to maximize in vitro transcription. A transcription factor in HeLa cells specifically bound to

and protected a GC rich sequence or GC...
... assays, and DNAse I and DMS footprinting assays. The protected GC-box had the consensus sequence of a high affinity binding site for the trans-*activating* factor SP1. The GC-box also formed the distal element of a tandem SP1-like motif, 21 bp upstream of the active TATA box. Synthetic *oligonucleotides* containing the GC-box specifically bound a HeLa factor and also depressed in vitro transcription from the B19 promoter when added as a competitor. Although...

... box. In vitro transcriptional activity decreased when the GC-box upstream of the B19 promoter was modified by site specific mutagenesis. Preliminary identification of other *cis*-*activating* motifs, which include two sequences recognized by factors that are functional both in transcription and replication, suggested that the B19 promoter is a complex regulatory...
?